

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: February 16, 2005, 15:52:54 / Search time 41 Seconds  
(without alignments)

1182.762 Million cell updates/sec

Title: US-09-808-124b-6

Sequence: 1 MTINIEDHRLHETSKEPDV.....LPPEGLQHNCUNSLRLIN 504

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 79:\*

1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description         |
|------------|--------|-------------|--------|----------|---------------------|
| 1          | 2652   | 98.8        | 1199   | 1 GNMVIM | HIV-1 retrovirus    |
| 2          | 2609   | 97.2        | 1204   | 2 S70393 | pol polyprotein -   |
| 3          | 2593   | 96.6        | 1204   | 2 S35475 | pol polyprotein -   |
| 4          | 2574   | 95.9        | 1196   | 1 GNMVGV | HIV-1 retrovirus    |
| 5          | 2541   | 94.7        | 1196   | 1 GNMVAV | HIV-1 retrovirus    |
| 6          | 2059.5 | 76.7        | 1784   | 2 T10532 | gag-pol polyprotein |
| 7          | 1949.5 | 72.6        | 1189   | 1 GNMVW7 | HIV-1 retrovirus    |
| 8          | 1893   | 70.5        | 1165   | 1 GNMVGL | HIV-1 retrovirus    |
| 9          | 1888.5 | 70.4        | 1046   | 1 GNMVCE | pol polyprotein -   |
| 10         | 1372   | 51.1        | 843    | 1 GNMVCK | pol polyprotein -   |
| 11         | 1130   | 42.1        | 559    | 2 A46311 | gag-pol polyprotein |
| 12         | 778.5  | 29.0        | 1751   | 2 S08442 | pol polyprotein     |
| 13         | 669    | 24.9        | 476    | 2 S08442 | probable pol prote  |
| 14         | 433    | 16.1        | 122    | 4 T01781 | pol polyprotein -   |
| 15         | 431.5  | 16.1        | 1157   | 1 GNMVJL | pol polyprotein -   |
| 16         | 430.5  | 16.0        | 958    | 2 S15566 | pol protein - siml  |
| 17         | 428.5  | 16.0        | 958    | 2 S15566 | hypothetical prote  |
| 18         | 416    | 15.5        | 1236   | 2 B35329 | retrovirus-related  |
| 19         | 412    | 15.4        | 1059   | 2 B24872 | probable retroviral |
| 20         | 403    | 15.0        | 1611   | 2 G84493 | probable retroviral |
| 21         | 399    | 14.9        | 949    | 2 D84487 | probable retroviral |
| 22         | 397    | 14.8        | 1182   | 2 T29097 | pro-pol-dutpase po  |
| 23         | 381.5  | 14.2        | 886    | 1 T07863 | pol polyprotein -   |
| 24         | 377.5  | 14.1        | 871    | 2 T07863 | probable polyprote  |
| 25         | 375    | 14.0        | 1333   | 2 S38635 | blatopria polyprot  |
| 26         | 374.5  | 14.0        | 1058   | 1 S34639 | retrovirus-related  |
| 27         | 373    | 13.9        | 1040   | 2 S34639 | gag, pol and env p  |
| 28         | 370.5  | 13.8        | 2272   | 2 T18572 | pol polyprotein ho  |
| 29         | 365    | 13.6        | 1045   | 2 S23570 |                     |

|    |       |      |      |          |                      |
|----|-------|------|------|----------|----------------------|
| 30 | 364.5 | 13.6 | 1060 | 2 T43046 | retrovirus-related   |
| 31 | 357   | 13.3 | 1745 | 2 S44816 | P44B2.1 protein -    |
| 32 | 351   | 13.1 | 1313 | 2 T29193 | hypothetical prote   |
| 33 | 348.5 | 13.0 | 1398 | 2 T18350 | probable pol polypr  |
| 34 | 343.5 | 12.8 | 1542 | 2 T17459 | pol polyprotein - to |
| 35 | 340   | 12.7 | 1009 | 2 S64734 | retrovirus-related   |
| 36 | 337   | 12.6 | 1295 | 2 S60179 | pol polyprotein ho   |
| 37 | 335   | 12.5 | 895  | 2 S35429 | pol polyprotein -    |
| 38 | 335   | 12.5 | 982  | 1 GNLJH2 | pol polyprotein -    |
| 39 | 335   | 12.5 | 1217 | 2 T13936 | pol protein - fnu1   |
| 40 | 335   | 12.5 | 1240 | 2 T04193 | hypothetical prote   |
| 41 | 334.5 | 12.5 | 895  | 1 GNFVIR | pol polyprotein -    |
| 42 | 333   | 12.4 | 896  | 2 S48613 | pol polyprotein -    |
| 43 | 332.5 | 12.4 | 1603 | 2 A48613 | gag/pol polyprotei   |
| 44 | 332   | 12.4 | 896  | 2 S48613 | pol polyprotein -    |
| 45 | 330.5 | 12.3 | 399  | 4 A45689 | retrovirus-related   |

#### ALIGNMENTS

##### RESULT 1

GNMVIM HIV-1 retrovirus (EC 3.4.23.16) - Moloney murine leukemia virus

N/Contains: nuclease (EC 3.1.-.-); retrovirus (EC 3.4.23.16); RNA-directed DNA polymer

C/Species: Moloney murine leukemia virus

A/Note: host Mus spp. (mouse)

C/date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 03-Jun-2002

C/accession: A03956

R/Shimnick, T.M.; Lerner, R.A.; Sutcliffe, J.G.

Nature 293, 545-548, 1981

A/Title: Nucleotide sequence of Moloney murine leukemia virus.

A/Reference number: A93265; MUID:82035843; PMID:6169994

A/accession: A03956

A/molecule type: genomic RNA

A/residues: 1-1199 <SH1>

A/experimental source: clone pMLV-1

A/Note: the pol polyprotein contains reverse transcriptase (about 80,000 daltons) and i

t yet been defined

C/Comment: This protein is synthesized as a gag-pol polyprotein.

C/genetics:

A/gene: pol

C/superfamily: pol polyprotein

C/keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; revers

F.3-102/Product: retrovirus #status predicted <RTP>

F.27/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 98.8%; Score 2652; DB 1; Length 1199;

Best Local Similarity 99.8%; Pred. No. 6.7e-187;

Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MTINIEDHRLHETSKEPDVLSGSTWLSDFPOAMETGGMGLAVQAPLITPLKATSTPV | 60  |
| DB | 120 | LTINIEDHRLHETSKEPDVLSGSTWLSDFPOAMETGGMGLAVQAPLITPLKATSTPV | 179 |
| QY | 61  | SIKQVPMQEARLGIKPIQRLDQGLVPCSPMNTPLPVKKEGTYDYPVDLREVN      | 120 |
| DB | 180 | SIKQVPMQEARLGIKPIQRLDQGLVPCSPMNTPLPVKKEGTYDYPVDLREVN      | 239 |
| QY | 121 | KRVEDIHTVNPYNLLSGLPSSHOWYTVLDKAFCLRLHPTSQPLFAFWRDPENG     | 180 |
| DB | 240 | KRVEDIHTVNPYNLLSGLPSSHOWYTVLDKAFCLRLHPTSQPLFAFWRDPENG     | 299 |
| QY | 181 | SGQLTWLTPGFGKNSPLTFEALHRLADRIQHPDILLYVYVDLLAATSELDCCOG    | 240 |
| DB | 300 | SGQLTWLTPGFGKNSPLTFEALHRLADRIQHPDILLYVYVDLLAATSELDCCOG    | 359 |
| QY | 241 | TRALLQTLGNLGYRSAAKQIQCKQVYLLGLLKEGQWLTFAKRTVMGPTPTKTRQ    | 300 |
| DB | 360 | TRALLQTLGNLGYRSAAKQIQCKQVYLLGLLKEGQWLTFAKRTVMGPTPTKTRQ    | 419 |
| QY | 301 | LRFLGTAGFCRLWIPGFAEWAPLYPLTKGTLLFNMGPDOCKAVOEIKQALLTPALCL | 360 |

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OM protein - protein search, using sw model

Run on: February 16, 2005, 15:52:54 ; Search time 181 Seconds

(without alignments)  
1425.900 Million cell updates/sec

Title: US-09-808-124B-6

Perfect score: 2684

Sequence: 1 MTLNIEDRHRLHETSKEPDV.....LPLEBGLQHNCIDNSRLIN 504

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_03.\*

1: uniprot\_prot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 2652   | 98.8        | 1199   | 1     | POL_MLVMO   |
| 2          | 2652   | 98.8        | 1737   | 2     | O92808      |
| 3          | 2652   | 98.2        | 1738   | 2     | O8UN00      |
| 4          | 2652   | 97.4        | 1204   | 2     | O41250      |
| 5          | 2652   | 97.3        | 1736   | 2     | O72J76      |
| 6          | 2609   | 97.2        | 1204   | 1     | POL_MLVFF   |
| 7          | 2605   | 97.1        | 1204   | 2     | O9YK99      |
| 8          | 2593   | 96.6        | 1204   | 1     | POL_MLVFP   |
| 9          | 2587   | 96.4        | 1738   | 2     | O39735      |
| 10         | 2583   | 96.2        | 1204   | 1     | POL_MLVFS   |
| 11         | 2579   | 96.1        | 1733   | 2     | O9S7M1      |
| 12         | 2576   | 96.0        | 1734   | 2     | O7SVK7      |
| 13         | 2571   | 95.8        | 1734   | 2     | O9J8E2      |
| 14         | 2568   | 95.7        | 1196   | 1     | POL_MLVAV   |
| 15         | 2567.5 | 95.7        | 1736   | 2     | O83362      |
| 16         | 2567   | 95.6        | 1734   | 2     | P70355      |
| 17         | 2552   | 95.1        | 1196   | 2     | O90RL4      |
| 18         | 2541   | 94.7        | 1196   | 1     | POL_MLVVD   |
| 19         | 2504   | 93.3        | 1180   | 2     | O9WHV7      |
| 20         | 2295   | 89.2        | 1038   | 2     | O83398      |
| 21         | 2198.5 | 81.9        | 626    | 2     | O72L06      |
| 22         | 2191.5 | 81.7        | 626    | 2     | O72L04      |
| 23         | 2181.5 | 81.3        | 1204   | 2     | O7ZKZ7      |
| 24         | 2127.5 | 79.3        | 1204   | 2     | O7ZKZ9      |
| 25         | 2125.5 | 79.2        | 1204   | 2     | O7ZKZ5      |
| 26         | 2075.5 | 77.4        | 1786   | 2     | O88811      |
| 27         | 2058.5 | 76.7        | 1784   | 2     | O88521      |
| 28         | 1945.5 | 72.6        | 1189   | 1     | POL_BAEVM   |
| 29         | 1945.5 | 72.5        | 868    | 2     | O73505      |
| 30         | 1945.5 | 72.5        | 2376   | 2     | O9Q1X5      |
| 31         | 1944.5 | 72.4        | 1146   | 2     | O8UM96      |

| Result ID | Score  | Query Match | Length | DB ID | Description |
|-----------|--------|-------------|--------|-------|-------------|
| 32        | 1944.5 | 72.4        | 1718   | 2     | O8J4V8      |
| 33        | 1944.5 | 72.4        | 1720   | 2     | O8J4V6      |
| 34        | 1943.5 | 72.4        | 1195   | 2     | O90RL6      |
| 35        | 1942.5 | 72.4        | 2378   | 2     | O9Q1X4      |
| 36        | 1941.5 | 72.3        | 2376   | 2     | O9Q1X3      |
| 37        | 1940.5 | 72.3        | 1145   | 2     | O9XSN8      |
| 38        | 1936.5 | 72.1        | 1144   | 2     | O8UM99      |
| 39        | 1933.5 | 72.0        | 1193   | 2     | O90RL9      |
| 40        | 1929.5 | 71.9        | 1146   | 2     | O8UM95      |
| 41        | 1929.5 | 71.9        | 1127   | 2     | O9TTC1      |
| 42        | 1903   | 70.9        | 1203   | 2     | O88815      |
| 43        | 1898   | 70.7        | 1127   | 2     | O70652      |
| 44        | 1893   | 70.5        | 1165   | 1     | POL_GALV    |
| 45        | 1888.5 | 70.4        | 1046   | 1     | POL_FENV1   |

## ALIGNMENTS

| Result ID | Score   | Query Match                       | Length | DB ID | Description |
|-----------|---|-----------------------------------|--------|-------|-------------|
| AC        | P03355  | STANDARD                          | PRT    | 1199  | AA.         |
| DT        | 21-JUL-1986   | (Rel. 01, Created)                |        |       |             |
| DT        | 01-FEB-1996   | (Rel. 33, Last sequence update)   |        |       |             |
| DT        | 25-OCT-2004   | (Rel. 45, Last annotation update) |        |       |             |
| DE        | Pol polyprotein [Contains: Protease (EC 3.4.23.-); Reverse transcriptase/RNase H (EC 2.7.7.49) (EC 3.1.26.4) (RT);            |                                   |        |       |             |
| DE        | Integrase (IN)].  |                                   |        |       |             |
| GN        | Name=POL;   |                                   |        |       |             |
| OS        | Moloney murine leukemia virus.  |                                   |        |       |             |
| OC        | Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.  |                                   |        |       |             |
| OX        | NCBI_Taxid=11801;   |                                   |        |       |             |
| RN        | [1]   |                                   |        |       |             |
| RP        | SEQUENCE FROM N.A. (CLONE PMLV-1).  |                                   |        |       |             |
| RX        | MEDLINE=82035843; PubMed=6169994;   |                                   |        |       |             |
| RA        | Shimnick R.M., Lerner R.A., Sutcliffe J.G.;   |                                   |        |       |             |
| RT        | "Nucleotide sequence of Moloney murine leukemia virus."   |                                   |        |       |             |
| RL        | Nature 293:543-548 (1981).  |                                   |        |       |             |
| RN        | [2]   |                                   |        |       |             |
| RP        | X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 130-394.   |                                   |        |       |             |
| RX        | MEDLINE=96097395; PubMed=8535782; DOI=10.1016/S0969-2126(01)00223-4;  |                                   |        |       |             |
| RA        | Georgiadis M.M., Jensen S.M., Ogata C.M., Telenitsky A., Goff S.P.,   |                                   |        |       |             |
| RT        | Hendrickson W.A.;   |                                   |        |       |             |
| RL        | "Mechanistic implications from the structure of a catalytic fragment of Moloney murine leukemia virus reverse transcriptase." |                                   |        |       |             |
| CC        | Structure 3:879-892 (1995).   |                                   |        |       |             |
| CC        | - FUNCTION: During replicative cycle of retroviruses, the reverse-  |                                   |        |       |             |
| CC        | transcribed viral DNA is integrated into the host chromosome by   |                                   |        |       |             |
| CC        | the viral integrase enzyme. RNase H activity is associated with   |                                   |        |       |             |
| CC        | the reverse transcriptase.  |                                   |        |       |             |
| CC        | - CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-   |                                   |        |       |             |
| CC        | phosphomonoester.   |                                   |        |       |             |
| CC        | - CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  |                                   |        |       |             |
| CC        | + (dN) (N).   |                                   |        |       |             |
| CC        | - PTM: Specific enzymatic cleavages in vivo yield mature proteins.  |                                   |        |       |             |
| CC        | - MICELANEOUS: This protein is synthesized as a Gag-Pol   |                                   |        |       |             |
| CC        | polyprotein.  |                                   |        |       |             |
| CC        | - SIMILARITY: Belongs to the retroviruses Pol polyprotein family.   |                                   |        |       |             |
| CC        | - SIMILARITY: Contains 1 peptidase A2 domain.   |                                   |        |       |             |
| CC        | - SIMILARITY: Contains 1 reverse transcriptase domain.  |                                   |        |       |             |
| CC        | - SIMILARITY: Contains 1 RNase H domain.  |                                   |        |       |             |
| CC        | - This SWISS-PROT entry is copyright. It is produced through a collaboration  |                                   |        |       |             |
| CC        | between the Swiss Institute of Bioinformatics and the EMBL outstation -   |                                   |        |       |             |
| CC        | the European Bioinformatics Institute. There are no restrictions on its   |                                   |        |       |             |
| CC        | use by non-profit institutions as long as its content is in no way  |                                   |        |       |             |
| CC        | modified and this statement is not removed. Usage by and for commercial   |                                   |        |       |             |
| CC        | entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>      |                                   |        |       |             |
| CC        | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).   |                                   |        |       |             |
| DR        | EMBL, J02255; -; NOT ANNOTATED_CDS.   |                                   |        |       |             |
| DR        | PDB, 1DIU; X-ray; A-I44-398.  |                                   |        |       |             |

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## OM protein - protein search, using sw model

Run on: February 16, 2005, 15:53:10 ; Search time 43 Seconds

(without alignments)  
874,956 Million cell updates/sec

Title: US-09-808-124B-6

Perfect score: 2684  
Sequence: 1 MTLNIEDHRLHETSKEPDV.....LPPEBGLQNCIDNSRLIN 504Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/SA\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/SB\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/SA\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/SB\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfillset.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description                            |
|------------|--------|-------------|--------|-------|--|
| 1          | 2652   | 98.8        | 1737   | 4     | US-09-309-572-13 Sequence 13, Appl     |
| 2          | 2652   | 98.8        | 1737   | 4     | US-09-718-096-13 Sequence 13, Appl     |
| 3          | 2650   | 98.7        | 1079   | 2     | US-08-929-967-8 Sequence 8, Appl       |
| 4          | 2611   | 97.3        | 665    | 2     | US-08-929-967-7 Sequence 7, Appl       |
| 5          | 2027   | 75.5        | 379    | 3     | US-09-603-185-6 Sequence 6, Appl       |
| 6          | 1944.5 | 72.4        | 1194   | 4     | US-09-171-553B-5 Sequence 5, Appl      |
| 7          | 1903   | 70.9        | 1203   | 3     | US-09-075-272-4 Sequence 4, Appl       |
| 8          | 985.5  | 36.7        | 654    | 4     | US-08-979-847B-91 Sequence 91, Appl    |
| 9          | 985.5  | 36.7        | 768    | 4     | US-08-979-847B-89 Sequence 89, Appl    |
| 10         | 978.5  | 36.5        | 683    | 4     | US-08-979-847B-198 Sequence 198, Appl  |
| 11         | 978.5  | 36.5        | 683    | 4     | US-08-979-847B-200 Sequence 200, Appl  |
| 12         | 975.5  | 36.3        | 683    | 4     | US-08-979-847B-208 Sequence 208, Appl  |
| 13         | 975.5  | 36.3        | 683    | 4     | US-08-979-847B-210 Sequence 210, Appl  |
| 14         | 915.5  | 34.1        | 768    | 3     | US-09-120-653D-5 Sequence 5, Appl      |
| 15         | 345    | 12.9        | 995    | 5     | PCT-US95-04910-14 Sequence 14, Appl    |
| 16         | 337    | 12.6        | 65     | 6     | 5320958-16 Patent No. 5320958          |
| 17         | 337    | 12.6        | 65     | 6     | 5320958-16 Patent No. 5320958          |
| 18         | 336.5  | 12.5        | 917    | 4     | US-08-259-451-11 Sequence 11, Appl     |
| 19         | 319.5  | 11.9        | 146    | 4     | US-08-979-847B-109 Sequence 209, Appl  |
| 20         | 318.5  | 11.9        | 146    | 4     | US-08-979-847B-133 Sequence 133, Appl  |
| 21         | 317.5  | 11.8        | 146    | 4     | US-08-979-847B-132 Sequence 132, Appl  |
| 22         | 317.5  | 11.8        | 146    | 4     | US-08-979-847B-202 Sequence 202, Appl  |
| 23         | 316    | 11.8        | 1122   | 4     | US-09-248-796A-16374 Sequence 16374, A |
| 24         | 309.5  | 11.5        | 146    | 4     | US-08-979-847B-134 Sequence 134, Appl  |
| 25         | 288.5  | 10.7        | 1055   | 2     | US-08-659-251-5 Sequence 5, Appl       |
| 26         | 288.5  | 10.7        | 1055   | 2     | US-09-256-490-5 Sequence 5, Appl       |
| 27         | 288.5  | 10.7        | 1055   | 5     | PCT-US96-11445-5 Sequence 5, Appl      |

|    |       |      |      |   |                                       |
|----|-------|------|------|---|---------------------------------------|
| 28 | 282   | 10.5 | 143  | 4 | US-08-979-847B-199 Sequence 199, Appl |
| 29 | 282   | 10.5 | 143  | 4 | US-08-979-847B-203 Sequence 203, Appl |
| 30 | 281.5 | 10.5 | 1150 | 3 | US-09-238-303-9 Sequence 9, Appl      |
| 31 | 281.5 | 10.5 | 1150 | 4 | US-09-946-239-9 Sequence 9, Appl      |
| 32 | 281   | 10.5 | 1802 | 3 | US-09-322-478-18 Sequence 18, Appl    |
| 33 | 281   | 10.5 | 1802 | 4 | US-09-586-106D-18 Sequence 18, Appl   |
| 34 | 280.5 | 10.5 | 260  | 6 | 5320958-4 Patent No. 5320958          |
| 35 | 280.5 | 10.5 | 260  | 6 | 5320958-4 Patent No. 5320958          |
| 36 | 277   | 10.3 | 143  | 4 | US-08-979-847B-141 Sequence 141, Appl |
| 37 | 275   | 10.2 | 143  | 4 | US-08-979-847B-139 Sequence 139, Appl |
| 38 | 274   | 10.2 | 143  | 4 | US-08-979-847B-140 Sequence 140, Appl |
| 39 | 273   | 10.2 | 3080 | 6 | 5223423-4 Patent No. 5223423          |
| 40 | 273   | 10.2 | 3080 | 6 | 5223423-4 Patent No. 5223423          |
| 41 | 261.5 | 9.7  | 1031 | 3 | US-08-811-682-15 Sequence 15, Appl    |
| 42 | 258.5 | 9.6  | 146  | 4 | US-08-979-847B-204 Sequence 204, Appl |
| 43 | 249   | 9.3  | 1018 | 4 | US-09-206-551-46 Sequence 46, Appl    |
| 44 | 244.5 | 9.1  | 560  | 4 | US-10-205-641-1 Sequence 1, Appl      |
| 45 | 244.5 | 9.1  | 850  | 4 | US-09-952-060-2 Sequence 2, Appl      |

## ALIGNMENTS

RESULT 1  
US-09-309-572-13  
Sequence 13, Application US/09309572  
Patent No. 6440730  
GENERAL INFORMATION:  
APPLICANT: Heinrich-Pette-Institut  
TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV  
FILE REFERENCE: P50489  
CURRENT APPLICATION NUMBER: US/09/309,572  
CURRENT FILING DATE: 1999-05-11  
EARLIER APPLICATION NUMBER: DE 198 56 463  
EARLIER FILING DATE: 1998-11-26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 1737  
TYPE: PRT  
ORGANISM: Moloney murine leukemia virus  
FEATURES:  
OTHER INFORMATION: gag-pol protein  
US-09-309-572-13

| Query Match | Similarity  | Score        | Pred. No. | DB 4:      | Length |
|-------------|---|--------------|-----------|------------|--------|
| Best Local  | 99.8%   | 2652         | 4.6e-278  | 1737       |        |
| Matches     | 497   | Conservative | 1         | Mismatches | 0      |
| Indels      | 0   | Gaps         | 0         |            |        |
| 1           | MTLNIEDHRLHETSKEPDVLSGTWLSDFQAMLETGAMGLAVRQAPLITPLKATSTPV | 60           |           |            |        |
| 658         | LTNIEDHRLHETSKEPDVLSGTWLSDFQAMLETGAMGLAVRQAPLITPLKATSTPV  | 717          |           |            |        |
| 61          | SIKQPMQEARLGKPHIQRLDQGLVPCQSPWNTPLPVKKGNDYRPVQDLREVN      | 120          |           |            |        |
| 718         | SIKQPMQEARLGKPHIQRLDQGLVPCQSPWNTPLPVKKGNDYRPVQDLREVN      | 777          |           |            |        |
| 121         | KRVEDIHVTNPVNLISGLPSHOWTVLDKAFCLRLHPTSPQPLFAEHRDPEMGI     | 180          |           |            |        |
| 778         | KRVEDIHVTNPVNLISGLPSHOWTVLDKAFCLRLHPTSPQPLFAEHRDPEMGI     | 837          |           |            |        |
| 181         | SGQLTWRLPGQFNKSPFLFDEALHRLDADRIQHPDILLOVYDDLLAATSELDCCQG  | 240          |           |            |        |
| 838         | SGQLTWRLPGQFNKSPFLFDEALHRLDADRIQHPDILLOVYDDLLAATSELDCCQG  | 897          |           |            |        |
| 241         | TRALLQITGNIGYASAKAQICQKQVYLYLKEGQWLTARKETVMQOPTPKTPRQ     | 300          |           |            |        |
| 898         | TRALLQITGNIGYASAKAQICQKQVYLYLKEGQWLTARKETVMQOPTPKTPRQ     | 957          |           |            |        |
| 301         | LRBELGTAGPRLMIPGABMAAPLYPLTKGTPLFMNGPDDQKAYOEIKQALLTPALGL | 360          |           |            |        |
| 958         | LRBELGTAGPRLMIPGABMAAPLYPLTKGTPLFMNGPDDQKAYOEIKQALLTPALGL | 1017         |           |            |        |